
 WIRE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Msrch_pp protein - protein database search, using Smith-Waterman algorithm
 on: Wed Aug 20 09:44:12 1997; MasPar time 12.79 Seconds
 665.067 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-469-637A-2
 Description: (1-401) from US08469637A.pep (1 of 2)
 Perfect Score: 3030
 Sequence: 1 MNKLCCALVFLDISIKWTT.....QKLELMIGNOVQSVKISCL 401

Scoring table: PAM 150
 Gap 11

Searched: 59021 seqs, 21210388 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot34
 1:part8 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11

Statistics: Mean 48.313; Variance 81.174; scale 0.595
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description	Pred. No.
1	405	13.4	461	9	TNR2_HUMAN	1.33e-63
2	375	12.4	474	9	TNR2_MOUSE	9.05e-57
3	303	10.0	277	2	CD40_HUMAN	1.03e-40
4	294	9.7	289	2	CD40_MOUSE	9.50e-39
5	269	8.9	326	10	VT2_MOUSE	2.38e-33
6	265	8.7	415	9	TNR2_MOUSE	1.97e-32
7	260	8.6	325	10	VT2_SEVKA	1.70e-31
8	260	8.6	435	9	TNR2_HUMAN	1.97e-31
9	263	7.7	349	10	VC22_YARV	9.20e-26
10	221	7.3	454	9	TNR1_MOUSE	2.72e-23
11	220	7.3	461	9	TNR1_RAT	4.35e-23
12	215	7.1	416	6	NGFR_CHICK	4.53e-22
13	213	7.0	427	6	NGFR_HUMAN	1.15e-21
14	207	6.8	425	6	NGFR_RAT	1.87e-20
15	188	6.2	323	3	FASA_BOVIN	1.08e-16
16	186	6.1	461	9	TNR1_PIG	2.66e-16
17	178	5.9	595	2	CD30_HUMAN	9.30e-15
18	172	5.7	455	9	TNR1_HUMAN	1.29e-13
19	159	5.2	256	1	41BB_MOUSE	3.45e-11
20	159	5.2	260	2	CD27_HUMAN	3.45e-11
21	146	4.8	271	7	OX40_RAT	7.67e-09
22	144	4.8	272	7	OX40_MOUSE	1.73e-08

ALIGNMENTS

RESULT	ID	TNR2_HUMAN	STANDARD:	PRT:	461 AA.
23	141	4.7	277	7	OX40L RECEPTOR PRECUR
24	140	4.6	255	1	41BB_LIGAND RECEPTOR
25	137	4.5	327	3	FASA_MOUSE
26	134	4.4	250	2	CD27_MOUSE
27	134	4.4	335	3	FASA_HUMAN
28	124	4.1	103	10	VA53_VACCC
29	124	4.1	103	10	VA53_VACCC
30	115	3.8	360	11	YTH9_YEAST
31	110	3.6	535	3	D2_DICDI
32	105	3.4	2813	10	VWF_HUMAN
33	102	3.4	3084	6	LMAI_MOUSE
34	101	3.3	712	4	GFAL_CANAL
35	101	3.3	1122	11	VC3C_YEAST
36	100	3.3	1752	3	DESP_HUMAN
37	99	3.3	2670	11	YAO5_SCHPO
38	96	3.2	431	7	PHOR_SHIDY
39	98	3.2	494	7	PR31_YEAST
40	96	3.2	1104	9	SVY_YEAST
41	96	3.2	1203	10	XCPE_YENIA
42	96	3.2	1356	5	KAB7_YEAST
43	98	3.2	1947	6	PBM_MOUSE
44	96	3.2	3707	7	PBM_MOUSE
45	97	3.2	4092	3	DYHC_YEAST

OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 CC EUKARYOTA: PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90260639.
 RA SMITH C.A., DAVIS T., ANDERSON D., SOLAM L., BECKMANN M.P., JERRY R.,
 RA DOMER S.R., COSMAN D., GOODWIN R.G.:
 RL SCIENCE 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91045991.
 RA KOHNO T., BREMER M.T., BAKER S.L., SCHWARTZ P.E., KING M.W.,
 RA HALE K.K., SQUIRES C.H., THOMPSON R.C., VANNICE J.L.:
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 90349572.
 RA HELLER R.A., SONG K., ONASCH M.A., FISCHER W.H., CHANG D.,
 RA RINGOLD G.M.:
 RL PROC. NATL. ACAD. SCI. U.S.A. 87:6151-6155(1990).
 RN [4]
 RP SEQUENCE OF 27-31.
 RX MEDLINE: 90110215.
 RA ENGELMANN H., NOVICK D., WALLACH D.:
 RL J. BIOL. CHEM. 265:1531-1536(1990).
 RN [5]
 RP SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE: 91056048.
 RA LOETSCHER H., SCHLAGER E.J., LAHM H.-W., PAN Y.-C.E., LESSLAUER W.,
 RA BROCKHAUS M.:
 RL J. BIOL. CHEM. 265:20131-20138(1990).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE: 93016040.
 RA PENNICA D., LAM V.T., MIZE N.K., WEBER R.F., LEWIS M., FENDLY B.M.,
 RA LIPARI M.T., GOEDDEL D.V.:

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RL J. BIOL. CHEM. 267:21172-21178(1992).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M32315; G189186; -.
DR EMBL: M35857; G339752; -.
DR EMBL: M55994; G339758; -.
DR PIR: A35356; A35356.
DR PIR: A36007; A36007.
DR PIR: A36475; A36475.
DR PIR: B35010; B35010.
DR PIR: A23666; A23666.
DR HSSP: P19438; 1TNR.
DR MIM: 191191; -.
DR PROSITE: PS00652; TNFR-NGFR.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
KW PHOSPHORYLATION.
FT CHAIN 1 22
FT DOMAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT DOMAIN 39 201 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 76 4 X TNFR-CYS.
FT REPEAT 77 118 TNFR-CYS 1.
FT REPEAT 119 162 TNFR-CYS 2.
FT REPEAT 163 201 TNFR-CYS 3.
FT REPEAT 201 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 67 75 BY SIMILARITY.
FT DISULFID 75 93 BY SIMILARITY.
FT DISULFID 93 96 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 BY SIMILARITY.
FT CARBOHYD 193 193 POTENTIAL.
FT CONFLICT 141 141 R -> P (IN REF. 3).
FT CONFLICT 141 141 R -> M (IN REF. 1).
FT CONFLICT 196 196 A -> T (IN REF. 3).
FT CONFLICT 363 363
SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;

Query Match 13.4%; Score 405; DB 9; Length 461;
st Local Similarity 41.8%; Pred. No. 1,33e+63;
atches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
CC SEQUENCE FROM N.A.
RX MEDLINE: 91187885.
RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA WONG G.H., CHEN E.Y., GOEDEL D.V.,
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE: 91246168.
RA GOODWIN R.G., ANDERSON D., JERRY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
RL MOL. CELL. BIOL. 11:3020-3026(1991).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M60469; G198828; -.
DR EMBL: M59378; G202095; -.
DR PIR: B38634; B38634.
DR HSSP: P19438; 1TNR.
DR PROSITE: PS00652; TNFR-NGFR.
DR RECEPTOR: TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
KW SIGNAL.
FT CHAIN 1 22
FT DOMAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 289 474 POTENTIAL.
FT DOMAIN 39 203 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 4 X TNFR-CYS.
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 120 164 TNFR-CYS 2.
FT REPEAT 165 203 TNFR-CYS 3.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 68 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;

Query Match 12.4%; Score 375; DB 9; Length 474;
Best Local Similarity 41.5%; Pred. No. 9.05e+57;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
  (1)
CC SEQUENCE FROM N.A.
RX MEDLINE: 89356608.
RA STAMENKOVIC I., CLARK E.A., SEED B.;
RL EMOB J. 8:1403-1410(1989).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: X60592; G29851.
DR PIR: S04460; S04460.
DR MIM: 109535.
DR PROSITE: PS00652; TNFR_NGFR.
KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 277 CD40L RECEPTOR.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 277 POTENTIAL.
FT DOMAIN 216 277 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 4 X TNFR-CYS.
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT REPEAT 153 187 TNFR-CYS 4.
FT CARBOHYD 180 180 POTENTIAL.
SQ SEQUENCE 277 AA; 30619 MW; 3B284411 CRC32;

Query Match 10.08; Score 303; DB 2; Length 277;
Best Local Similarity 36.88; Pred. No. 1,03e-40;
Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;

Db 38 cdscpgqgkivsaqctefetecjpcgeselfdwrethqnhkycdpn-1glr-vqgkx 95
QY 41 CDKCPGGTYLKQHCITAKMKTVCAPCPDHYTDSMHTSDC-L--YCSPVCKELQYVKQEC 97
Db 96 tsecltctceegwhctseacescvlhrscspgfyvkqialtyvsdtlcepcpvgffsnvs 155
QY 98 NRTNHNVCCEKRGY-L-EL-EFCLKRRSCPPGFGVQAGTPERNYTCRCKRCPDGFSSNET 154
Db 156 safekchpwtscetkdlvvgagctnktdivcg 187
QY 155 SSKAPCRKHTNCVSFGLLTQKGNATHDNICS 186

*LT 4
CD40_MOUSE STANDARD: PRT; 289 AA.
P27512;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
GN CD40.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
  (1)
CC SEQUENCE FROM N.A.
RX MEDLINE: 92105763.
RA TORRES R.M., CLARK E.A.;
RL J. IMMUNOL. 148:620-626(1992).
  (2)
CC REVISIONS.
RC STRAIN-BALB/C;
RA TORRES R.M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-LIVER;
RX MEDLINE: 93094586.
RA GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,

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RA HOWARD M., COCKAYNE D.A.;
RL J. IMMUNOL. 149:3821-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M83312; G1553059.
DR EMBL: M84126; G192526.
DR EMBL: M84129; G192526; JOINED.
DR EMBL: M94128; G192526; JOINED.
DR EMBL: M94127; G192526; JOINED.
DR PIR: A46476; A46476.
DR HSSP: P19438; ITNR.
DR PROSITE: PS00652; TNFR_NGFR.
KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT CHAIN 1 19
FT SIGNAL 1 19
FT DOMAIN 20 289 CD40L RECEPTOR.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 289 POTENTIAL.
FT DOMAIN 216 289 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 4 X TNFR-CYS.
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT CARBOHYD 153 153 TNFR-CYS 4.
SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;

Query Match 9.7%; Score 294; DB 2; Length 289;
Best Local Similarity 38.88; Pred. No. 9.50e-39;
Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdscpgysrlstshctelxtqchpcdsgefsagwreilchqhthnepn-qglr-vkxgq 95
QY 41 CDKCPGGTYLKQHCITAKMKTVCAPCPDHYTDSMHTSDC-LY--CSPVCKELQYVKQEC 97
Db 96 taesclvccckegqhtsdcceacaghtpcilpgfyymematetdclvchpcpvgffsnvs 155
QY 98 NRTNHNVCCEKRGY-L-EL-EFCLKRRSCPPGFGVQAGTPERNYTCRCKRCPDGFSSNET 154
Db 156 slfekcypwtscedknlelvkqstgtnvlycg 187
QY 155 SSKAPCRKHTNCVSFGLLTQKGNATHDNICS 186

RESULT 5
ID VT2_MYXVL STANDARD: PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS MYXOMA VIRUS (STRAIN LAUSANNE).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXYIRINAE;
OC LEPORIPOVIRUSES.
RN [1]
CC SEQUENCE FROM N.A.
RX MEDLINE: 91335768.
RA UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
RL VIROLOGI 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL: M85181; G332310.
DR EMBL: A23729; E199442.
DR PIR: A40566; GOVZML.
DR HSSP: P19438; ITNR.
DR PROSITE: PS00652; TNFR_NGFR.
KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
FT CHAIN 1 16
FT SIGNAL 17 326 POTENTIAL T2.
FT DOMAIN 27 186 4 X TNFR-CYS.

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Query Match	8.7%;	Score 265;	DB 9;	Length 415;
Best Local Similarity	28.9%;	Pred. No. 1,70e-33;		
Matches	54;	Conservative	30;	Mismatches 92; Indels 11; Gaps 8;
FT DISULFID 104 124				BY SIMILARITY.
FT DISULFID 126 132				BY SIMILARITY.
FT DISULFID 139 150				BY SIMILARITY.
FT DISULFID 142 169				BY SIMILARITY.
FT DISULFID 172 187				BY SIMILARITY.
FT CARBOHYD 40 40				POTENTIAL.
FT CARBOHYD 179 179				POTENTIAL.
SO SEQUENCE 415 AA;				44956 MW; 305DD121 CRC32;
Query Match	8.7%;	Score 265;	DB 9;	Length 415;
Best Local Similarity	28.9%;	Pred. No. 1,70e-33;		
Matches	54;	Conservative	30;	Mismatches 92; Indels 11; Gaps 8;
Db 52 ephmdvccscipgpfefavcsisqdtvcktcphnsynehnhlsteqlcrp-cdlvlgf 110				
QY 34 ETSHQLCDKRCPCPTYLKQHCTAKMKITVCAPCPDHYVTDMSHTSDECLYCSPVCKE-LQY 92				
Db 111 eevaprcsdiiaetrcqpgmcsyldmecnvceeerlvlcqpgcreaeytdeimdtvncv 170				
QY 93 VK-OECNRTNHRVCEKEGR--YLELE-FCLKNR-S-CPFGGV-VQAGTPERNVCK 143				
Db 171 pckpghfqtcsapracqphtrceiqglveaapqtsycticknpepganllal11st 230				
QY 144 RCPGFGFSNENSSKAPCRKHNCSVFGULLTKQKNATHDNCSGNSSESTQKCGIDVILCE 203				
Db 231 vllflf 237				
QY 204 EAEFFRA 210				
RESULT 7				
ID VT2_SFVKA STANDARD; PRT; 325 AA.				
AC P25943;				
DT 01-MAY-1992 (REL. 22, CREATED)				
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)				
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)				
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).				
GN T2.				
OS SHOPE FIBROMA VIRUS (STRAIN KASZA) (SFV).				
OC VIRIDAE: DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXYIRINAE;				
OC LEPORIPVIRUSES.				
RN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE: 87321103.				
RA UPTON C., DELANGE A.M., MCFADDEN G.;				
RL VIROLOGY 160:20-30(1987).				
RN [2]				
RP FUNCTION.				
RX MEDLINE: 91207415.				
RA SMITH C.A., DAVIS T., MIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,				
RA MCFADDEN G., GOODWIN R.G.;				
RL BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).				
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO				
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL				
CC ANTI-VIRAL EFFECTS OF THE CYTOKINE.				
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.				
DR EMBL: M17433; -; NOT ANNOTATED_CDS.				
DR EMBL: A23727; E199408; -.				
DR PIR: B43692; B43692.				
DR HSSP: P19438; 11NR.				
DR PROSITE: PS00652; TNFR_NGFR.				
KM RECEPTOR, GLYCOPROTEIN; REPEAT; SIGNAL.				
FT SIGNAL 1 16				POTENTIAL.
FT CHAIN 17 325				POTENTIAL.
FT DOMAIN 27 186				PROTEIN T2.
FT REPEAT 27 62				4 X TNFR-CYS.
FT REPEAT 63 104				TNFR-CYS 1.
FT REPEAT 105 147				TNFR-CYS 2.
FT REPEAT 148 186				TNFR-CYS 3.
FT CARBOHYD 105 105				TNFR-CYS 4.
FT CARBOHYD 181 181				POTENTIAL.
FT CARBOHYD 205 205				POTENTIAL.
FT CARBOHYD 238 238				POTENTIAL.

01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFR1 OR TNFR-1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9187885.
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GEDEDEL D.V.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9124616.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RA MOL. CELL. BIOL. 11:3020-3026(1991).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9128501.
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
 RA GRAY P.W., FELDWMANN M., FOXWELL B.M.J.,
 RA EUR. J. IMMUNOL. 21:1649-1656(1991).
 [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE-SPLEEN.
 RX MEDLINE: 92039815.
 RA ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.,
 RA IMMUNOGENETICS 34:338-340(1991).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94245292.
 RA BEBO B.F., LINTHICUM D.S.,
 RA IMMUNOGENETICS 39:450-451(1994).
 [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93156721.
 RA ROTHE J., BLUTHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.,
 RA MOL. IMMUNOL. 30:165-175(1993).
 [7]
 RP FUNCTION: RECEPTOR FOR TNF-ALPHA.
 [8]
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 [9]
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: M60468; G198926; -;
 DR EMBL: M59377; G202097; -;
 DR EMBL: X59338; G53579; -;
 DR EMBL: X57796; G54849; -;
 DR EMBL: L26349; G430733; -;
 DR EMBL: M76556; G202102; -;
 DR EMBL: M88067; G202102; JOINED.
 DR EMBL: M76555; G202102; JOINED.
 DR PIR: A38634; GOMSTL.
 DR PIR: S16677; S16677.
 DR PIR: S19021; S19021.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS50017; DEATH_DOMAIN.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 RX SIGNAL 1 21
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 213 235 POTENTIAL.
 FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 356 441 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.

FT DISULFID 102 117 BY SIMILARITY.
 FT DISULFID 105 125 BY SIMILARITY.
 FT DISULFID 127 143 BY SIMILARITY.
 FT DISULFID 146 158 BY SIMILARITY.
 FT DISULFID 149 166 BY SIMILARITY.
 FT DISULFID 168 179 BY SIMILARITY.
 FT DISULFID 182 191 BY SIMILARITY.
 FT DISULFID 185 195 BY SIMILARITY.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 202 202 POTENTIAL.
 FT CONFLICT 394 394 R -> G (IN REF. 6).
 SQ SEQUENCE 454 AA; 50129 MW; 486EBC09 CRC32;
 SQ
 Query Match 7.38; Score 221; DB 9; Length 454;
 Best Local Similarity 33.18; Pred. No. 2,726-23;
 Matches 48; Conservative 21; Mismatches 65; Indels 11; Gaps 9;
 Db 49 yvshknsicctckhkylysdpspgrdvtcrecekgftaagnylrgclstcrke 108
 QY 31 YDEETSHQLDCKCPGTYLKHCHTAK-WKTVCAPCPDHYTDSWHSDECLYCSPVCKE 89
 Db 109 msqvelspcgadkdvccgkengfgylyselhfgvdcspcfnq-tvlipketqntvcn 167
 QY 90 LQYVK-QECNRTNHNVCCKGSG--RLV-DIEF-CLKHRSRCPGCGVQAQTPERNIVCK 143
 Db 168 -chagfflrescwpchckkneec 191
 QY 144 RCPDGFESNETSKA-P-CRKHTNC 166
 RESULT 11
 ID TNFR1_RAT STANDARD: PRT: 461 AA.
 AC P22934;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
 GN TNFR1 OR TNFR-1.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9109841.
 RA HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PEIZENMAIER K.,
 RA LANTZ M., OLSSON I., HUPPMANN R., STRATOWA C., ADOLF G.R.,
 RA DNA CELL BIOL. 9:705-715(1990).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M63122; G207362; -;
 DR PIR: B36585; B36585.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR PROSITE: PS50017; DEATH_DOMAIN.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 RX SIGNAL 1 21
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 234 POTENTIAL.
 FT DOMAIN 235 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 363 448 DEATH DOMAIN.
 FT DISULFID 44 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 81 BY SIMILARITY.
 FT DISULFID 84 99 BY SIMILARITY.
 FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 461 AA; 50969 MM; 82F68B08 CRC32;

Query Match 7.3%; Score 220; DB 9; Length 461;
Best Local Similarity 33.8%; Pred.No.4,35e-23;
Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db 49 yabphnsicctckhgylysdcpdpgevcvcdkgtftasqnhvrgclscckrke 108
1 YDEETSHOLLCDKCPGTYLKHCHTAK-WKTVCAPCPDHYTDSMHTSDECLYCSPPVCKE 89
109 mfyvetspcskadmtvsgcknqfgylysethfgcvdscpfng-tvllpckekvnc 167
90 L-QYVKQCEKRNTHNVCECK--E-GRYL-EIEF-CLKHRSCPPGCGVVOAGTPERNTVCK 143
OY 168 -chagffisgncpcshcknqec 191
OY 144 RCPDGF-S-NETSSKAPCRKHTNC 166

RESULT 12 STANDARD: PRT: 416 AA.
AC NGFR-CHICK
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LINGFR)
OC GALLUS GALLUS (CHICKEN).
OC EDURAROTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN.
RX MEDLINE; 9016579.
RA LANGE T.H., WESSAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
RA SHOOTER E.M., REICHARDT L.F.,
RA NEURON 2:1123-1134(1989).
RL [2]
SEQUENCE OF 21-416 FROM N.A.
MEDLINE; 90152140.
RA HEIDER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.,
RL DEV. BIOL. 137:287-304(1990).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
PIR: J00006; J00006.
PIR: A60504; A60504.
DR PROSITE; PS00652; TNFR-NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 416 NGF RECEPTOR.
FT DOMAIN 29 239 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 240 261 POTENTIAL.
FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 181 4 X TNFR-CYS.
FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT CARBOHYD 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 POTENTIAL.
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MM; 4D3F086A CRC32;

Query Match 7.1%; Score 215; DB 6; Length 416;
Best Local Similarity 30.4%; Pred.No.4,53e-22;
Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 ckaenlgeyvvpgcgvn-qvcepcldsvtsatpckpctq-cvylhmsapcve 93
OY 41 CDKCPGTYLKHCHTAKWKTVCAPCPDHY-YTDSMHTSDECLYCSPPVCKELOYKQCNR 99
Db 94 sdaavccrcaygyfdelsgsckeesicevfglmfpcrdsqdvceecpctgfsdeanf 153
OY 100 THNVCECKEKRYL-EIE-FCLKHRSCPPGCGVVOAGTPERNTVCKRCPDGFNETSK 157
Db 154 dpcplciceeneyvke-clatsdaec 180
OY 158 APCRKHNTGCVFGLLTQKGNATHDNIC 185

RESULT 13 STANDARD: PRT: 427 AA.
AC NGFR-HUMAN
AC P08138;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LINGFR).
GN NGFR.
OS HOMO SAPIENS (HUMAN).
OC EDURAROTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87051725.
RA JOHNSON D., LANAHAN A., BUCK C.R., SENGAL A., MORGAN C., MERCER E.,
RL CELL 47:545-554(1986).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
NT-3, AND NT-4.
CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
BOND FORMATION.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
PIR: M14764; G189205; .
PIR: A25218; G0HUN.
DR HSSP; P19438; ITNR.
DR MIM; 162010; .
DR PROSITE; PS00652; TNFR-NGFR.
DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KW PHOSPHORYLATION; SIGNAL.

Query Match	Best local Similarity	7.0%;	Score 213;	DB 6;	Length 427;
Matches 45;	Conservative 19;	Mismatches 60;	Indels 5;	Gaps 5;	
FT SIGNAL	1	28			
FT CHAIN	29	427			
FT DOMAIN	29	250			
FT TRANSMEM	251	272			
FT DOMAIN	273	427			
FT DOMAIN	31	189			
FT REPEAT	31	65			
FT REPEAT	66	107			
FT REPEAT	108	147			
FT REPEAT	148	189			
FT DOMAIN	344	421			
FT DISULFID	32	43			
FT DISULFID	44	57			
FT DISULFID	47	64			
FT DISULFID	67	83			
FT DISULFID	86	99			
FT DISULFID	89	107			
FT DISULFID	109	122			
FT DISULFID	125	138			
FT DISULFID	128	146			
FT DISULFID	149	164			
FT DISULFID	167	180			
FT DISULFID	170	188			
FT DOMAIN	197	248			
FT CARBOHYD	60	60			
SEQUENCE	427 AA;	45183 MW;	EE2924BD	CRC32;	
Query Match	Best local Similarity	7.0%;	Score 213;	DB 6;	Length 427;
Matches 45;	Conservative 19;	Mismatches 60;	Indels 5;	Gaps 5;	
44	cKacnlgsvagpcgan-qlvcepcldsvfisdvvsatepkpcte-cvqigsmsapcve	101			
41	CDKCPGRTYLKHCHTAKMTVCAPCPDHY-YDMSHTSDDECLYCSVPCKELQYKQCNR	99			
102	addavrcrcygygqdetlgrceaccrcvcaagslvtscqdkqntvceecpdtgdeanhv	161			
100	TNHRVCECKEGRYL-EI-EFCLKHRSCEPGGVAGIPERNVCKRCRCPDGFENETSSK	157			
162	deolpctve	170			
158	APCRKHTNC	166			
RESULT 14					
ID NGFR.RAT	STANDARD:	PRT:	425 AA.		
AC P07174:					
01-APR-1988 (REL. 07, CREATED)					
01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)					
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)					
LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)					
DE (GPR80-LNGFR).					
GN NGFR.					
OS RATTUS NORVEGICUS (RAT).					
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
OC EUTHERIA; RODENTIA.					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE; 87115859.					
RA RADEKE M.J., MISSO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;					
RL NATURE 325:593-597(1987).					
RP (2)					
RC SEQUENCE OF 1-22 FROM N.A.					
RX TISSUE-LIVER;					
RA MEDLINE; 93077038.					
RL METSIS M., TIMMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;					
CC GENE 121:247-254(1992).					
-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,					
CC NT-3, AND NT-4.					
-1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE					
CC BOND FORMATION.					
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.					
CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.					

CC	-1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
DR	EMBL; X05137; G56756; -; NOT_ANNOTATED_CDS.
DR	EMBL; X61269; -; NOT_ANNOTATED_CDS.
DR	PIR; A26431; A26431.
DR	HSSP; P19438; 1TNR.
DR	PROSITE; PS00652; TNFR_NGR.
DR	PROSITE; PS0017; DEATH_DOMAIN.
KW	RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
KV	PHOSPHORYLATION; SIGNAL.
FT	SIGNAL 1 29
FT	CHAIN 30 425
FT	DOMAIN 30 251
FT	TRANSMEM 252 273
FT	DOMAIN 274 425
FT	DOMAIN 32 190
FT	REPEAT 32 66
FT	REPEAT 67 108
FT	REPEAT 109 148
FT	REPEAT 149 190
FT	DOMAIN 198 249
FT	DOMAIN 354 419
FT	DISULFID 33 44
FT	DISULFID 45 58
FT	DISULFID 48 65
FT	DISULFID 68 84
FT	DISULFID 87 100
FT	DISULFID 90 108
FT	DISULFID 110 123
FT	DISULFID 126 139
FT	DISULFID 129 147
FT	DISULFID 150 165
FT	DISULFID 168 181
FT	DISULFID 171 189
FT	CARBOHYD 61
FT	CARBOHYD 71
SO	SEQUENCE 425 AA; 45432 MW; 7D78F258 CRC32;
	Query Match 6.8%; Score 207; DB 6; Length 425;
	Best Local Similarity 33.3%; Pred.No.1.87e-20;
	Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;
Dd	45 kcaclngsgvqvgpgan-qlycepcldnvtstsvsatcpkpte-clqlgsmaspve 102
Oy	41 CDKCPGGTYLQHGCTAKKRTVCAPCPDHY-VTDMSHTSGDELYCSPCKELQYVKOCNR 99
Dd	103 addavcraygyydeedghceacsvcgslftscgdkgntcceepctgsdaanhv 162
Oy	100 TNNRYCECKEGRIEIE-FCLKHRCPPGPGVVQAGIPERNIVCKKCPDGFFSNETSSK 157
Dd	163 dpcldpctvc 171
Oy	158 APCRKHTNC 166
RESULT 15	
ID	FASA_BOVIN STANDARD; PRG: 323 AA.
AC	P51867;
DT	01-OCT-1996 (REL. 34, CREATED)
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE	FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE	(APO-1 ANTIGEN) (CD95).
GN	APLI OR FAS.
OS	BOS TAURUS (BOVINE).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; ARTIODACTILA.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE; 96226401.
RL	YOO J.; STONE R.T.; BEATTIE C.W.:
RL	DNA CELL BIOL. 15:227-234(1996).
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

